

# **Hang Chang**

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## **Education**

- Ph.D. Pattern Recognition and Artificial Intelligence, June 2008, Institute of Automation, Chinese Academy of Sciences
- B.S. Automatic Control, June 2003, Huazhong University of Sciences and Technology, China

## **Research Interests**

- Developing computational platform for:
  - Multidimensional profiling of phenotypic responses on multiple scales;
  - Identification of subpopulations from phenotypic responses;
  - Identification of micro-environmental cues and intrinsic genetic events that predict each subpopulation;
- High performance computing
- Image processing, pattern recognition and machine learning with applications in computational biology

## **Research Statement**

Presently, I am a project scientist in Life Sciences Division, Lawrence Berkeley National Laboratory. I have been working closely with collaborators at UC San Francisco and UC Berkeley. I am the lead developer of (i) a high performance system for characterizing tissue histopathology [9, 25]; (ii) a high performance system for quantitative analysis of breast density [3]; and (iii) a high performance system for characterizing membrane-bound macromolecules [4, 15, 17]. And I am also a co-developer of (i) a high performance system for characterizing microtubule in plant cell wall [27]; (ii) a system for identifying subpopulations from morphometric data and their association with genome-wide array data [9]; (iii) a system for quantitative analysis of 3D multicellular systems [5]. I have published several papers on quantitative analysis of both 2D and 3D assays imaged with bright-field microscopy, electronic microscopy and fluorescent microscopy. Given my diverse experience in working with image-based assays and genome-wide array data, I believe that I can make a strong contribution to (i) developing algorithms for invariant representation from spatio-temporal data, (ii) developing advanced methods in machine learning for recognition and classification of biological entities, and (iii) analyzing and integrating results using custom bioinformatics tools.

## **Professional Experience**

- 2008~Present Project Scientist, Lawrence Berkeley National Laboratory  
Electrical Engineering - Imaging and Bioinformatics
- 2006~2007 Research Assistant, Lawrence Berkeley National Laboratory  
Electrical Engineering - Imaging and Bioinformatics
- 2003~2005 Research Assistant, Institute of Automation, Chinese Academy of Sciences

## Publications

- **Journal Paper (Peer-reviewed)**

1. B. Parvin, Q. Yang, J. Han, H. Chang, B. Rydberg, and M. H. Barcellos-Hoff, "Iterative Voting for Inference of Structural Saliency and Characterization of Subcellular Events", IEEE Trans. on Image Processing, vol. 16, no. 3, pp. 615-623, March 2007.
2. H. Chang, Q. Yang, and B. Parvin, "Segmentation of heterogeneous blob objects through voting and level set formulation", Pattern Recognition Letters, 28(13):1781-1787, October 2007.
3. H. Chang, Rosa Anna DeFilippis, Thea D. Tlsty, Bahram Parvin, "Graphical methods for quantifying macromolecules through bright field imaging", Bioinformatics 25(8): 1070-1075, 2009
4. J. Han, H. Chang, K. Andarawewa, P. Yaswen, M.H. Barcellos-Hoff, B. Parvin, "Multidimensional Profiling of Cell Surface Proteins and Nuclear Markers", IEEE/ACM Trans. on Computational Biology and Bioinformatics, vol. 7, no. 1, pp. 80-90, Jan. 2010.
5. J. Han, H. Chang, O. Giricz, G.Y. Lee, F.L. Baehner, J.W. Gray, M.J. Bissell, P.A. Kenny, B. Parvin, "Molecular Predictors of 3D Morphogenesis by Breast Cancer Cell Lines in 3D Culture", PLoS Computational Biology, vol. 6, no. 2, Feb. 2010.
6. Katarzyna A. Rejniak, Shizhen E. Wang, Nicole S. Bryce, H. Chang, Bahram Parvin, Jerome Jourquin, Lourdes Estrada, Joe W. Gray, Carlos L. Arteaga, Alissa M. Weaver, Vito Quaranta, Alexander R. A. Anderson, "Linking Changes in Epithelial Morphogenesis to Cancer Mutations Using Computational Modeling", PLoS Computational Biology, 6(8), 2010.
7. J. Han, H. Chang, Q. Yang, G. Fontenay, T. Groesser, M.H. Barcellos-Hoff, and B. Parvin, "Multiscale Iterative Voting for Differential Analysis of Stress Response for 2D and 3D Cell Culture Models", Journal of Microscopy, vol. 241, no.3, pp. 315-326, 2011.
8. T. Groesser, H. Chang, G. V. Fontenay, J. Chen, SV. Costes, M.H. Barcellos-Hoff, B. Parvin, B. Rydberg, "Persistence of γ-H2AX and 53BP1 foci in proliferating and non-proliferating human mammary epithelial cells after exposure to γ-rays or iron ions", Int J Radiat Biol., vol. 87, no. 7, pp. 696-710, 2011
9. H. Chang, G. V. Fontenay, J. Han, G. Cong, F. L. Baehner, J. W. Gray, P. T. Spellman and B. Parvin, "Morphometric Analysis of TCGA Glioblastoma Multiforme", BMC Bioinformatics, vol. 12, no. 484, 2011
10. S. Nath, V. A. Spencer, J. Han, H. Chang, K. Zhang, G. V. Fontenay, C. Anderson, J. M. Hyman, Marit Nilsen-Hamilton, Young-Tae Chang, and B. Parvin, "Identification of fluorescent compounds with non-specific binding property via high throughput live cell microscopy", PloS One, vol. 7, no. 1, 2012.

- **Conference Paper (Peer-reviewed)**

11. J. Han, H. Chang, Q. Yang, M.H. Barcellos-Hoff, and B. Parvin, "3D Segmentation of Mammospheres for Localization Studies", Proc. IEEE International Symposium on Visual Computing, vol. 1, pp. 518-527, Nov. 2006.
12. H. Chang, Q. Yang, Chunhong Pan, "An Iterative Bayesian Approach for Digital Matting", International Conference on Pattern Recognition, vol. 2, pp.122-125, 2006

13. J. Han, H. Chang, Q. Yang, M.H. Barcellos-Hoff, and B. Parvin, "Segmentation of Mammosphere Structures from Volumetric Data", Proc. IEEE International Symposium on Biomedical Imaging, pp. 524-527, April 2007.
14. H. Chang, Q. Yang, M. Auer, and B. Parvin, "Modeling of Front Evolution with Graph Cut Optimization", International Conference on Image Processing, vol. 1, pp. 241-244, 2007.
15. H. Chang, K.L. Andarawewa, J. Han, M.H. Barcellos-Hoff, and B. Parvin, "Perceptual Grouping of Membrane Signals in Cell-based Assays", Proc. IEEE International Symposium on Biomedical Imaging, pp. 532-535, April 2007.
16. H. Chang, C. Park and B. Parvin, "Quantitative Representation of Three-dimensional Cell Culture Models", IEEE International Symposium on Biomedical Imaging, pp. 89-92, April 2007.
17. J. Han, H. Chang, P. Yaswen, M.H. Barcellos-Hoff, and B. Parvin, "Integrated profiling of cell surface protein and nuclear marker for discriminant analysis", Proc. IEEE International Symposium on Biomedical Imaging, pp. 1342-1346, May 2008.
18. H. Chang, R.A. DeFilippis, T.D. Tlsty, and B. Parvin, "Scoring Histological Sections through Immunohistochemistry", IEEE International Symposium on Biomedical Imaging, pp. 344-347, 2008.
19. H. Chang, Q. Yang, and B. Parvin, "A Bayesian Approach for Image Segmentation with Shape Priors", IEEE Conference on Computer Vision and Pattern Recognition, pp. 1-8, 2008.
20. Q. Wen, H. Chang, and B. Parvin, "A Delaunay Triangulation Approach for Segmenting Clumps of Nuclei", IEEE International Symposium on Biomedical Imaging, pp. 9-12, 2009.
21. J. Han, H. Chang, G. Fontenay, N. Wang, J.W. Gray, and B. Parvin, "Morphometric Subtyping for a Panel of Breast Cancer Cell Lines", Proc. IEEE International Symposium on Biomedical Imaging, pp. 791-794, Jun. 2009.
22. H. Chang, M. Auer, and B. Parvin, "Structural Annotation of EM Images by Graph Cut", IEEE International Symposium on Biomedical Imaging, pp. 1103-1106, 2009.
23. H. Chang and B. Parvin, "Multiphase Level Set for Automated Delineation of Membrane-bound Proteins", IEEE International Symposium on Biomedical Imaging, pp. 165-168, 2010.
24. J. Han, H. Chang, L. A. Loss, K. Zhang, F. L. Baehner, J. W. Gray, P. T. Spellman, B. Parvin, "Comparison of sparse coding and kernel methods for histopathological classification of glioblastoma multiforme", IEEE International Symposium on Biomedical Imaging, pp. 711-714, 2011.
25. H. Chang, Leandro A. Loss, Paul T. Spellman, Alexander Borowsky and Bahram Parvin, "Batch-Invariant Nuclear Segmentation in Whole Mount Histology Sections", IEEE International Symposium on Biomedical Imaging, 2012.
26. Ju Han, Hang Chang, Gerald V. Fontenay, Paul Spellman, Alexander Borowsky and Bahram Parvin, "Molecular Bases of Morphometric Composition in Glioblastoma Multiforme", IEEE International Symposium on Biomedical Imaging, 2012.
27. Leandro Loss, Hang Chang, Purbasha Sarkar, Manfred Auer and Bahram Parvin, "Detection of 3D Filamentous Networks From Tomographic Electron Microscopy", IEEE International Symposium on Biomedical Imaging, 2012.

- **Papers Under Review**

1. Multi-Reference Level Set for Nuclear Segmentation in Glioblastoma Multiforme.
2. Multi-Reference Graph Cut (MRGC) for Modeling and Characterizing Tumor Histopathology in Glioblastoma Multiforme
3. CD36 Repression Activates a Multicellular Stromal Program Shared by High Mammographic Density and Tumor Tissues
4. Automatic Segmentation and Quantification of Filamentous Structures in Electron Tomography
5. Multi-phase Level Set for Delineation of Membrane-bound Macromolecules

## **Professional Services**

Member of IEEE (Institute of Electrical and Electronics Engineers)

Reviewer for

IEEE Transactions on Image Processing  
Journal of Medical Plants Research  
BMC Bioinformatics  
Machine Vision and Applications

## **Programming**

Proficiency with C++, Matlab, R, MySQL, PHP

## Referees

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